STIC Search Report
Biotech-Chem Library

USPTO

TO: Patrick S Riggins Location: REM-2D60&2C70 Art Unit: 1633 Monday, April 10, 2006 Case Serial Number: 10/500173	From: Toby Port Location: Biotech-Chem Library REM-1A59 Phone: 571-272-2523 toby.port@uspto.gov

Search Notes

Examiner Riggins,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Toby Port
X22523

sira
Search and Information
Resources Administration

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              GenCore version 5.1.7
         Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on:      April  9, 2006, 02:10:27 ; Search time 344.814 Seconds
                                       (without alignments)
                                       6758.955 Million cell updates/sec

Title:           US-10-500-173-1
Perfect score:   41
Sequence:        1 gaaacaatgacacaatcagc.......cccaataccaagggcctgac 41

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        5883141 seqs, 2842172653 residues

Total number of hits satisfying chosen parameters:      11766282

Minimum DB seq length:  0
Maximum DB seq length:  2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :    GenEmbl:*
        *
        1:  gb_ba:*
        2:  gb_in:*
        3:  gb_env:*
        4:  gb_om:*
        5:  gb_ov:*
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        7:  gb_ph:*
        8:  gb_pr:*
        9:  gb_ro:*
       10:  gb_sts:*
       11:  gb_sy:*
       12:  gb_un:*
       13:  gb_vi:*
       14:  gb_htg:*
       15:  gb_pl:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	41	100.0	41	6	BD181246	Cell spec
2	41	100.0	41	6	BD182147	Cell spec
3	41	100.0	260	6	BD181247	Cell spec
4	41	100.0	260	6	BD182148	Cell spec
5	41	100.0	314	8	HS12H4R	54537 H.sapiens C
6	41	100.0	333	6	BD181248	Cell spec
7	41	100.0	333	6	BD182149	Cell spec
8	41	100.0	1221	8	D85611-	D85611 Human smoot
9	41	100.0	142645	8	AC008481	AC008481 Homo sapi
10	41	100.0	178488	14	AC151856	AC151856 Papio ham
11	41	100.0	224294	14	AC151861	AC151861 Colobus g
12	39.4	96.1	163264	14	AC151891	AC151891 Callicebu
13	39.4	96.1	181714	14	AC151893	AC151893 Aotus nan
14	39.4	96.1	186803	14	AC151868	AC151868 Callithri
15	39.4	96.1	199562	14	AC163457	AC163457 Bos tauru
16	39.4	96.1	250810	14	AC151886	AC151886 Saimiri b
17	37.8	92.2	236017	14	AC150437	AC150437 Lemur cat
18	36.2	88.3	485	9	AF123268	Rattus no

19	36.2	88.3	1216	9	MMCALP01	Mus musculu
20	36.2	88.3	3001	9	MMU37071	Mus musculu
21	36.2	88.3	10373	9	MUSH1CA	Mus musculu
22	36.2	88.3	174533	14	AC073718	AC073718 Mus muscu
23	36.2	88.3	178594	14	AC144892	AC144892 Didelphis
24	36.2	88.3	194267	14	AC163623	AC163623 Mus muscu
c 25	36.2	88.3	195294	14	AC051623	AC051623 Mus muscu
26	36.2	88.3	201371	14	AC073786	AC073786 Mus muscu
c 27	36.2	88.3	236685	14	AC084744	AC084744 Mus muscu
c 28	36.2	88.3	245942	14	AC132792	AC132792 Rattus no
c 29	34.6	84.4	207823	14	AC145542	AC145542 Oryctolag
30	34.6	84.4	230705	14	AC130996	AC130996 Rattus no
c 31	25.2	62.4	230705	8	AC110760	AC110760 Homo sapi
c 32	24.2	59.0	171632	8	AC124604	AC124604 Mus muscu
c 33	24.2	59.0	220801	9	AC095809	AC095809 Rattus no
c 34		58.5	263827	14	BA000031_19	Continuation (20 o
c 35	23.6	57.6	110000	1	BA000031_19	Continuation
c 36	23.6	57.6	133128	9	BX276083	BX276083 Zebrafish
37	23.6	57.6	149630	14	CR628386	CR628386 Danio rer
38	23.6	57.6	153943	14	AC027417	AC027417 Homo sapi
c 39	23.6	57.6	157544	8	AC098590	AC098590 Homo sapi
40	23.2	56.6	170143	14	AC048384	AC048384 Homo sapi
41	23.2	56.6	58259	14	AC148218	AC148218 Medicago
c 42	23.2	56.6	209156	14	AC114696	AC114696 Rattus no
c 43	23.2	56.6	214942	9	AC125214	AC125214 Mus muscu
44	23.2	56.6	227767	14	AC118766	AC118766 Rattus no
c 45	23	56.1	228506	14	AC111714	AC111714 Rattus no
			9990	1	AE002243	AE002243 Chlamydop

ALIGNMENTS

```
RESULT 1
BD181246
LOCUS       BD181246               41 bp    DNA            linear   PAT 15-MAY-2003
DEFINITION  Cell specific express replication vector.
ACCESSION   BD181246
VERSION     BD181246.1  GI:30792164
KEYWORDS    JP 2002335965-A/1.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 41)
  AUTHORS   Takahashi,K., Yamamura,H. and Miyatake,S.
  TITLE     Cell specific express replication vector
  JOURNAL   Patent: JP 2002335965-A 1 26-NOV-2002;
            JAPAN SCIENCE AND TECHNOLOGY CORP
  OS        Homo sapiens (human)
  PN        JP 2002335965-A/1
  PD        26-NOV-2002
  PF        14-MAY-2001 JP 2001143999
  PI        KATSUHITO TAKAHASHI,HISAKO YAMAMURA,SHINICHI MIYATAKE PC
COMMENT     C12N15/09,A61K35/76,A61K35/76,A61K48/00,A61P35/00,C12N5/10,C12N15/00, PC
            C12N5/00
  CC        Cell specific express replication vector
  FH        Key             Location/Qualifiers
  FT        source          1..41
  FT                        /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1..41
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
ORIGIN

Query Match        100.0%;  Score 41;  DB 6;  Length 41;
Best Local Similarity   100.0%;  Pred. No. 7.7e-06;
Matches  41;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy        1 GAAACAATGACACAATCAGCTCCAATACCAAGGGCCTGAC 41
            ||||||||||||||||||||||||||||||||||||||||
```

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                    GenCore version 5.1.7
         Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on:    April  9, 2006, 02:04:37 ; Search time 59.4306 Seconds
                                       (without alignments)
                                 4597.840 Million cell updates/sec

Title:           US-10-500-173-1
Perfect score:   41
Sequence:        1 gaaacaatgacacaatcagc.........cccaataccaaggggcctgac 41

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters:          9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :    N Geneseq_21:*
              1: geneseqm1980s:*
              2: geneseqm1990s:*
              3: geneseqm2000s:*
              4: geneseqm2001as:*
              5: geneseqm2001bs:*
              6: geneseqm2002as:*
              7: geneseqm2002bs:*
              8: geneseqm2003as:*
              9: geneseqm2003bs:*
             10: geneseqm2003cs:*
             11: geneseqm2003ds:*
             12: geneseqm2004as:*
             13: geneseqm2004bs:*
             14: geneseqm2005s:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the total score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

c	Result No.	Score	% Score	Match	Query Length	DB	ID	Description
	1	41	100.0	41		10	ADC21270	Adc21270 Human cel
	2	41	100.0	41		10	ADD68309	Add68309 Human ang
	3	41	100.0	41		10	ADD29393	Add29393 Antiarter
	4	41	100.0	41		10	ABZ70044	Abz70044 Oligonucl
	5	41	100.0	41	260	10	ADC21271	Adc21271 Human cel
	6	41	100.0	41	260	10	ADD68310	Add68310 Human ang
	7	41	100.0	41	260	10	ADD29394	Add29394 Antiarter
	8	41	100.0	41	260	10	ABZ70045	Abz70045 Oligonucl
	9	41	100.0	41	333	10	ADC21272	Adc21272 Human cal
	10	41	100.0	41	333	10	ADD68311	Add68311 DNA compr
	11	41	100.0	41	333	10	ADD29395	Add29395 Human cal
	12	41	100.0	41	333	10	ABZ70046	Abz70046 Human cal
c	13	23	56.1		110000	8	AAX91990_11	Continuation (12 o
c	14	22.2	54.1		780	8	ACA40205	Aca40205 Prokaryot
	15	22	53.7		652	2	AAX19896	Aax19896 Mouse pro
	16	22	53.7		2293	2	AAX19900	Aax19900 Plasmid p
c	17	21.8	53.2		86276	11	ACN43942	Acn43942 Human gen
	18	21.6	52.7		16131	10	ADF77178	Adf77178 KALPA gen
	19	21.4	52.2		1209	9	ADB85463	Adb85463 Streptoco
	20	21.4	52.2		1212	9	ADB85471	Adb85471 Streptoco
c	21	21.4	52.2		4226	4	ABL08190	Abl08190 Drosophil
	22	21.4	52.2		110000	14	AEA61163_2	Continuation (3 of
	23	21.2	51.7		957	8	ABX92193	Abx92193 Human ova
	24	21.2	51.7		1460	13	ABX92194	Abx92194 Human ova
	25	21.2	51.7		64125	13	ABD33295	Abd33295 Human can
	26	21	51.2		396	8	ABX47703	Abx47703 Bovine ES
	27	21	51.2		403	8	ABX40611	Abx40611 Bovine ES
c	28	21	51.2		417	3	AAC41719	Aac41719 Arabidops
c	29	21	51.2		616	3	AAC44877	Aac44877 Arabidops
	30	21	51.2		753	8	ABX05433	Abx05433 Human nov
	31	21	51.2		803	6	ABQ26745	Abq26745 Oligonucl
c	32	21	51.2		803	6	ABQ26744	Abq26744 Oligonucl
c	33	21	51.2		972	5	AAS66748	Aas66748 DNA encod
	34	21	51.2		973	6	ABN74450	Abn74450 Bovine em
	35	21	51.2		974	6	ABN74449	Abn74449 Bovine em
	36	21	51.2		1270	2	AAZ24855	Aaz24855 Human sec
c	37	21	51.2		11445	4	AAK70537	Aak70537 Human imm
	38	21	51.2		46830	14	ADZ12773	Adz12773 Human can
	39	21	51.2		55235	4	AAK67426	Aak67426 Human imm
c	40	21	51.2		73930	12	ADQ97577	Adq97577 Human can
c	41	21	51.2		86574	6	ABK83560	Abk83560 Human cDN
	42	21	51.2		86574	13	ADR52822	Adr52822 Drug ther
c	43	20.8	50.7		180	6	ABQ95988	Abq95988 Tumour su
c	44	20.8	50.7		199	6	ABQ95990	Abq95990 Tumour su
c	45	20.8	50.7		199	6	ABQ95984	Abq95984 Tumour su

ALIGNMENTS

```
RESULT 1
ADC21270
ID   ADC21270 standard; DNA; 41 BP.
XX
AC   ADC21270;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Human cell-specific expression vector-related DNA sequence #1.
XX
KW   human; cell-specific expression vector; cell-specific replication vector;
KW   gene therapy; malignant tumour; liver fibrosis; postoperative stenosis;
KW   organ transplantation; arteriosclerosis; diabetic omentopathy; ds.
XX
OS   Homo sapiens.
XX
PN   WO200305788B-A1.
XX
PD   17-JUL-2003.
XX
PF   26-DEC-2002; 2002WO-JP013683.
XX
PR   28-DEC-2001; 2001JP-00402102.
PR   30-AUG-2002; 2002JP-00255395.
XX
PA   (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
PI   Takahashi K, Yamamura H;
XX
DR   WPI; 2003-577527/54.
XX
PT   Cell-specific expression/replication vector containing transcription
PT   initiation regulating domain of human calponin gene, applicable in gene
PT   therapy of malignant tumor lung and liver fibrosis or diabetic
PT   omentopathy.
XX
PS   Claim 2; SEQ ID NO 1; 66pp; Japanese.
XX
CC   The invention comprises a cell-specific expression/replication vector
CC   which does not act on normal cells. The vector of the invention is useful
CC   in gene therapy for the treatment of: malignant tumour, liver fibrosis,
CC   postoperative stenosis (e.g. stenosis after organ transplantation),
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                    GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on:      April  9, 2006, 02:12:09 ; Search time 421.382 Seconds
                                         (without alignments)
                                         4552.334 Million cell updates/sec

Title:            US-10-500-173-1
Perfect score:    41
Sequence:         1 gaaacaatgacacaatcagc........cccaataccaaggggcctgac 41

Scoring table:    IDENTITY_NUC
                  Gapop 10.0 , Gapext 1.0

Searched:         41078325 seqs, 2339541228 residues

Total number of hits satisfying chosen parameters:    82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing:  Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

Database :

        BST:*
         1: gb_est1:*
         2: gb_est2:*
         3: gb_est3:*
         4: gb_htc:*
         5: gb_est4:*
         6: gb_est5:*
         7: gb_est6:*
         8: gb_est7:*
         9: gb_gss1:*
        10: gb_gss2:*
        11: gb_gss3:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
c 1	24.2	59.0	578	9	AZ954724	2M0220I01
c 2	24.2	59.0	687	2	BB636361	BB636361
c 3	24.2	59.0	817	8	CX705842	gmrtDrNS0
4	24	58.5	578	2	BG887927	EST513778
c 5	23.2	56.6	455	8	W81232	zd85g07.s1
c 6	23.2	56.6	457	8	DN589073	49998.1 L
c 7	23.2	56.6	457	8	DR037737	49998.2 L
c 8	23.2	56.6	457	8	DR037738	49998.3 L
c 9	23.2	56.6	465	1	AI773494	EST254594
c 10	23.2	56.6	580	1	AI170292	EST216218
c 11	23.2	56.6	624	2	BG598900	EST503788
c 12	23.2	56.6	736	3	BQ046841	EST595959
c 13	23	56.1	403	6	CD002122	EST0119 N
c 14	23	56.1	429	6	CD603495	RZ148A3B0
c 15	23	56.1	444	3	BM403754	zam6160 Z
c 16	23	56.1	486	5	BW881674	BW881674
c 17	23	56.1	489	2	BG799583	fo08h03.y
c 18	23	56.1	571	9	AQ891537	HS_3063 A
c 19	23	56.1	644	6	CB343759	CA32EN0O0
c 20	23	56.1	732	6	CF232494	PtadX0001
c 21	23	56.1	760	9	BZ773739	mcv78b08.
c 22	23	56.1	1246	10	AG341458	Mus muscu
c 23	22.8	55.6	628	6	CB577767	AMGNNUC:U
c 24	22.8	55.6	697	10	CW332222	104_829_1
25	22.8	55.6	750	10	CW332223	104_829_1
26	22.6	55.1	420	8	DR91045	EST11085B
27	22.6	55.1	822	9	B2988727	PUGHP34TB
28	22.6	55.1	861	9	CC350006	OGIAX91TH
c 29	22.6	55.1	869	10	CG106814	PUFVE86TB
c 30	22.6	55.1	883	10	CL292836	ZMMBBB064
c 31	22.6	55.1	908	9	CC364981	PUBEC65TD
32	22.4	54.6	137	5	BU035599	QHJ7H13.y
33	22.4	54.6	233	5	BG591195	EST499037
34	22.4	54.6	323	8	DN842758	KECB32-27
35	22.4	54.6	358	7	CO908605	BJ02033B1
36	22.4	54.6	386	9	AQ061197	CIT-HSP-2
c 37	22.4	54.6	402	11	CR490303	mth2-1610
c 38	22.4	54.6	424	11	CR038246	Forward s
c 39	22.4	54.6	425	11	CR259602	Forward s
40	22.4	54.6	438	2	BB343332	EST408481
41	22.4	54.6	453	2	BB344046	EST409208
42	22.4	54.6	474	6	CA847544	EST0452 C
43	22.4	54.6	478	5	BU021048	QHE29C11.
44	22.4	54.6	487	7	CO911511	BJ03020B1
45	22.4	54.6	490	2	BB920230	EST423999

ALIGNMENTS

```
RESULT 1
AZ954724/c
LOCUS       AZ954724               578 bp    DNA     linear   GSS 27-APR-2001
DEFINITION  2M0220I01R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
            clone UUGC2M0220I01 R, genomic survey sequence.
ACCESSION   AZ954724
VERSION     AZ954724.1  GI:13825951
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
            1 (bases 1 to 578)
REFERENCE   1 (bases 1 to 578)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,K., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000    Std Error: 0.00
            Plate: 0220   row: I  column: 01
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 578.
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0220I01"
                     /sex="Female"
                     /lab_host="E. coli strain X110-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC2M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
```

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                GenCore version 5.1.7
         Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on:    April 8, 2006, 13:46:44 ; Search time 20.1767 Seconds
                                     (without alignments)
                           3612.096 Million cell updates/sec

Title:          US-10-500-173-1
Perfect score:  41
Sequence:       1 gaaacaatgacaccaatcagc........cccaataccaaggcctgac 41

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters:     2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      Issued_Patents NA:*
                1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*
                2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
                3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
                4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
                5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*
                6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*
                8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
                9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Query Length	DB	ID	Description
1		41	100.0	15585	3	US-09-949-016-11927	Sequence 11927, A
2		41	100.0	15585	3	US-09-949-016-15627	Sequence 15627, A
3		23	56.1	1230025	3	US-09-198-452A-1	Sequence 1, Appli
4		23	56.1	1230230	3	US-09-438-185A-1	Sequence 1, Appli
5	c	21.8	53.2	601	3	US-09-949-016-130708	Sequence 130708, A
6	c	21.8	53.2	42250	3	US-09-949-016-15426	Sequence 15426, A
7	c	21.6	52.7	601	3	US-09-949-016-196661	Sequence 196661, A
8		21.6	52.7	28585	3	US-09-949-016-17311	Sequence 17311, A
9	c	21	51.2	209210	3	US-09-949-016-15094	Sequence 15094, A
10	c	20.8	50.7	456	3	US-09-328-352-82	Sequence 82, Appl
11	c	20.8	50.7	601	3	US-09-949-016-103354	Sequence 103354,
12	c	20.8	50.7	601	3	US-09-949-016-103355	Sequence 103355,
13	c	20.8	50.7	601	3	US-09-949-016-127545	Sequence 127545,
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; Sequence 11927, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
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; SEQ ID NO 11927
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; ORGANISM: Human
; FEATURE:
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; LOCATION: (1)...(15585)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-11927

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; Sequence 15627, Application US/09949016
; Patent No. 6812339
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; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
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          Copyright (c) 1993 - 2006 Bioacceleration Ltd.

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; TITLE OF INVENTION: Replication Vector Showing Cell-Specific Expression
; FILE REFERENCE: K01002PCT
; CURRENT APPLICATION NUMBER: US/10/477,797
; CURRENT FILING DATE:  2003-11-13
; PRIOR APPLICATION NUMBER: JP P2001-143999
; PRIOR FILING DATE: 2001-05-14
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
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;   LENGTH: 41
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; Publication No. US20050032214A1
; GENERAL INFORMATION:
; APPLICANT: Katsuhito TAKAHASHI
; APPLICANT: Hisako YAMAMURA
; TITLE OF INVENTION: Cell specific expression/replication vector
; FILE REFERENCE: 4439-4022
; CURRENT APPLICATION NUMBER: US/10/500,173
; CURRENT FILING DATE:  2004-06-24
; PRIOR APPLICATION NUMBER: JP P2001-402102
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: JP P2002-255395
; PRIOR FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
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; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-20
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
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; PRIOR FILING DATE: 2001-01-16
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GenCore version 5.1.7
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9	188.2	72.4	178488	14	AC151856	AC151856 Papio ham
10	184.6	71.0	186803	14	AC151868	AC151868 Callithri
11	181.4	69.8	181714	14	AC151893	AC151893 Aotus nan
12	179.8	69.2	250810	14	AC151886	AC151886 Saimiri b
13	178.2	68.5	163264	14	AC151891	AC151891 Callicebu
c 14	168.4	64.8	236017	14	AC150437	AC150437 Lemur cat
15	164	63.1	1600	8	BC022015	BC022015 Homo sapi
16	164	63.1	1605	6	CS119457	CS119457 Sequence
17	150	57.7	1633	8	BC036307	BC036307 Homo sapi
c 18	142	54.6	199562	14	AC163457	AC163457 Bos tauru

c 19	134.2	51.6	207823	14	AC145542	AC145542 Oryctolag
c 20	101	38.8	245942	14	AC132792	AC132792 Rattus no
21	100	38.5	1522	6	E11061	E11061 Calponin ge
22	93.6	36.0	10373	9	MUSH1CA	L49022 Mus musculu
23	93.6	36.0	174533	14	AC073718	AC073718 Mus muscu
c 24	93.6	36.0	194267	14	AC163623	AC163623 Mus muscu
25	93.6	36.0	195294	14	AC051623	AC051623 Mus muscu
26	93.6	36.0	201371	14	AC073786	AC073786 Mus muscu
c 27	93.6	36.0	236685	14	AC084744	AC084744 Mus muscu
28	92	35.4	1517	6	AX330146	AX330146 Sequence
29	92	35.4	1517	8	AX337316	AX337316 Sequence
30	92	35.4	1517	8	D17408	D17408 Homo sapien
31	87.4	33.6	485	9	AF123268	AF123268 Rattus no
32	84.2	32.4	3001	9	MMU37071	U37071 Mus musculu
33	78	30.0	1500	6	CQ724324	CQ724324 Sequence
34	78	30.0	1504	6	AX146871	AX146871 Sequence
35	78	30.0	1504	6	AX578072	AX578072 Sequence
36	78	30.0	1504	8	HSU37019	U37019 Homo sapien
37	77	29.6	1521	8	AK223234	AK223234 Homo sapi
38	76.2	29.3	156	6	CQ503702	CQ503702 Sequence
39	76.2	29.3	711	6	CQ482594	CQ482594 Sequence
40	74	28.5	1496	8	S80560	S80560 basic calpo
41	58	22.3	178594	14	AC144892	AC144892 Didelphis
42	56.6	21.8	1216	9	MMCALP01	U38929 Mus musculu
43	46.2	17.8	165072	14	AC145332	AC145332 Felis cat
c 44	41.6	16.0	177950	8	AC019103	AC019103 Homo sapi
45	41	15.8	41	6	BD181246	BD181246 Cell spec

ALIGNMENTS

RESULT 1
BD181247
LOCUS   BD181247   260 bp   DNA   linear   PAT 15-MAY-2003
DEFINITION   Cell specific express replication vector.
ACCESSION   BD181247
VERSION   BD181247.1 GI:30792165
KEYWORDS   JP 2002335965-A/2.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
               Hominidae; Homo.
REFERENCE   1 (bases 1 to 260)
AUTHORS   Takahashi,K., Yamamura,H. and Miyatake,S.
TITLE   Cell specific express replication vector
JOURNAL   Patent: JP 2002335965-A 2 26-NOV-2002;
               JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT   OS Homo sapiens (human)
               PN JP 2002335965-A/2
               PD 26-NOV-2002
               PF 14-MAY-2001 JP 2001143999
               PI KATSUHITO TAKAHASHI,HISAKO YAMAMURA,SHINICHI MIYATAKE PC
               C12N15/09,A61K35/76,A61K48/00,A61P35/00,C12N5/10,C12N15/00,PC
               C12N5/00
               CC Cell specific express replication vector
FEATURES   Location/Qualifiers
FH   Key   Location/Qualifiers
FT   source   1..260
FT   /organism='Homo sapiens (human)'.
FEATURES   Location/Qualifiers
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ORIGIN

Query Match   100.0%; Score 260; DB 6; Length 260;
Best Local Similarity   100.0%; Pred. No. 6e-57;
Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 GAAACAATGACACAATCAGCTCCCCAATACCAAGGGCCTGACTACCAAGGAGCGAGGGGAAG 60
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               GenCore version 5.1.7
        Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on:  April 9, 2006, 02:04:37 ; Search time 376.877 Seconds
                                    (without alignments)
                                    4597.840 Million cell updates/sec

Title:          US-10-500-173-2
Perfect score:  260
Sequence:       1 gaaacaatgacacaatcagc.........gccagagcccaccggccagc 260

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters:   9993994

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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                 Listing first 45 summaries

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                9: geneseqm2003bs:*
               10: geneseqm2003cs:*
               11: geneseqm2003ds:*
               12: geneseqm2004as:*
               13: geneseqm2004bs:*
               14: geneseqm2005s:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Match Length	DB	ID	Description
1		260	100.0	260	10	ADC21271	Adc21271 Human cel
2		260	100.0	260	10	ADD68310	Add68310 Human ang
3		260	100.0	260	10	ADD29394	Add29394 Antiarter
4		260	100.0	260	10	ABZ70045	Abz70045 Oligonucl
5		260	100.0	333	10	ADC21272	Adc21272 Human cal
6		260	100.0	333	10	ADD68311	Add68311 DNA compr
7		260	100.0	333	10	ADD29395	Add29395 Human cal
8		260	100.0	333	10	ABZ70046	Abz70046 Human cal
9		213	81.9	1206	13	ACN41242	Acn41242 Human dia
10		213	81.9	1257	13	ACN41241	Acn41241 Human dia
11		213	81.9	1395	13	ACN41239	Acn41239 Human dia
12		213	81.9	1395	13	ACN41240	Acn41240 Human dia
13		164	63.1	1605	12	ADN04009	Adn04009 Antipsori
14		135	51.9	1586	10	ADJ56427	Adj56427 Human cDN
15		100	38.5	1522	2	AAQ86719	Aaq86719 Carponin
16		100	38.5	1522	2	AAT18663	Aat18663 Carponin
17		92	35.4	1517	6	ABL62318	Abl62318 Colon ade
18		92	35.4	1517	6	ABL69488	Abl69488 Prostate
19		92	35.4	1517	6	ABT10830	Abt10830 Human bre
20		78	30.0	78	12	ADQ83552	Adq83552 Human tum
21		78	30.0	78	4	AAD07354	Aad07354 Human DNA
22		78	30.0	78	8	ABZ34836	Abz34836 Coding se
23		78	30.0	78	13	ADB75245	Adb75245 Prostate
24		78	30.0	78	13	ADR99030	Adr99030 Calponin
25		76.2	29.3	156	5	ABV35551	Abv35551 Human pro
26		76.2	29.3	711	5	ABV14470	Abv14470 Human pro
27		41	15.8	41	10	ADC21270	Adc21270 Human cel
28		41	15.8	41	10	ADD68309	Add68309 Human ang
29		41	15.8	41	10	ADD29393	Add29393 Antiarter
30		41	15.7	41	10	ABZ70044	Abz70044 Oligonucl
31	c	40.8	15.7	158001	12	ADL17884	Adl17884 Human pho
32		39.8	15.3	425	9	ACH30634	Ach30634 Human tes
33		39.4	15.2	648	9	ABV05301	Abv05301 Human pro
34	c	37.6	14.5	142299	10	ADD50651	Add50651 BAC seque
35	c	37.6	14.5	142299	14	ADV77909	Adv77909 Human BAC
36	c	37.4	14.4	3195	8	ABX75327	Abx75327 Human cDN
37	c	37.4	14.4	3195	8	AAD52555	Aad52555 FZD 8 DNA
38		37.4	14.4	3195	8	ABZ81827	Abz81827 Receptor
39	c	37.4	14.4	3195	10	ADB75319	Adb75319 Prostate
40	c	37.4	14.4	3195	11	ADN39809	Adn39809 Cancer/an
41	c	37.4	14.4	3195	12	ADO22267	Ado22267 Human FZD
42	c	37.4	14.4	3195	13	ADR46635	Adr46635 Cancer-as
43	c	37.4	14.4	3195	14	ADX16340	Adx16340 DNA encod
44	c	37.4	14.4	3205	12	ADQ24577	Adq24577 Human sof
45	c	37.4	14.4	3206	12	ADM86913	Adm86913 Human pro

ALIGNMENTS

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RESULT 1
ADC21271
ID   ADC21271 standard; DNA; 260 BP.
XX
AC   ADC21271;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Human cell-specific expression vector-related DNA sequence #2.
XX
KW   human; cell-specific expression vector; cell-specific replication vector;
KW   gene therapy; malignant tumour; liver fibrosis; postoperative stenosis;
KW   organ transplantation; arteriosclerosis; diabetic omentopathy; ds.
XX
OS   Homo sapiens.
XX
PN   WO2003057888-A1.
XX
PD   17-JUL-2003.
XX
PF   26-DEC-2002; 2002WO-JP013683.
XX
PR   28-DEC-2001; 2001JP-00402102.
PR   30-AUG-2002; 2002JP-00255395.
XX
PA   (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
PI   Takahashi K, Yamamura H;
XX
DR   WPI; 2003-577527/54.
XX
PT   Cell-specific expression/replication vector containing transcription
PT   initiation regulating domain of human calponin gene, applicable in gene
PT   therapy of malignant tumor lung and liver fibrosis or diabetic
PT   omentopathy.
XX
PS   Claim 3; SEQ ID NO 2; 66pp; Japanese.
XX
CC   The invention comprises a cell-specific expression/replication vector
CC   which does not act on normal cells. The vector of the invention is useful
CC   in gene therapy for the treatment of: malignant tumour, liver fibrosis,
CC   postoperative stenosis (e.g. stenosis after organ transplantation),
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                    GenCore version 5.1.7
          Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on:    April  9, 2006, 02:12:09 ; Search time 2672.18 Seconds
                               (without alignments)
                               4552.334 Million cell updates/sec

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Perfect score: 260
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched:      41078325 seqs, 2339351228 residues

Total number of hits satisfying chosen parameters:    82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

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2	164	63.1	596	2	BG720683	BG720683 602692572
3	152	58.5	789	3	BI831662	BI831662 603078806
4	112.4	43.2	577	3	BI831410	BI831410 603074509
5	103	39.6	300	1	AU099476	AU099476 AU099476
6	103	39.6	580	3	BP257909	BP257909 BP257909
7	103	39.6	580	3	BP343021	BP343021 BP343021
8	103	39.6	581	3	BP216801	BP216801 BP216801
9	103	39.6	581	3	BP375335	BP375335 BP375335
10	103	39.6	582	3	BP262111	BP262111 BP262111
11	103	39.6	582	3	BP311382	BP311382 BP311382
12	103	39.6	582	3	BP329165	BP329165 BP329165
13	103	39.6	582	3	BP330989	BP330989 BP330989
14	103	39.6	582	3	BP331068	BP331068 BP331068
15	103	39.6	583	3	BP329772	BP329772 BP329772
16	103	39.6	588	3	BP329527	BP329527 BP329527
17	103	39.6	791	1	AU136287	AU136287 AU136287
18	103	39.6	874	1	AU122686	AU122686 AU122686
19	102	39.2	778	8	CX756920	CX756920 AGENCOURT
20	102	39.2	930	5	BU526756	BU526756 AGENCOURT
21	101.4	39.2	580	3	BP372922	BP372922 BP372922
22	101.4	39.0	583	3	BP330966	BP330966 BP330966
23	101	38.8	566	3	BP261780	BP261780 BP261780
24	99.8	38.4	582	3	BP206459	BP206459 BP206459
25	97	37.3	581	3	BP328199	BP328199 BP328199
26	94.2	36.2	471	7	CN366947	CN366947 170004241
27	92	35.4	582	3	BP377953	BP377953 BP377953
28	91	35.0	646	7	CN366953	CN366953 170005999
29	91	35.0	1444	4	CR620483	CR620483 full-leng
30	90	34.6	742	8	CX752039	CX752039 AGENCOURT
31	88.4	34.0	832	5	BX374338	BX374338 BX374338
32	88.2	33.9	762	8	CX753789	CX753789 AGENCOURT
33	88.2	33.9	1086	5	BM553077	BM553077 AGENCOURT
34	88	33.8	660	1	AL046845	AL046845 DKFZp586B
35	88	33.8	706	1	AL046846	AL046846 DKFZp586B
36	87.4	33.6	714	1	AL046924	AL046924 DKFZp586H
37	87	33.5	996	3	BI771104	BI771104 603059679
38	86.4	33.2	700	1	AL533558	AL533558 AL533558
39	86	33.1	942	5	BU838479	BU838479 AGENCOURT
40	85	32.7	493	8	R13007	R13007 yf71c02.r1
41	85	32.7	545	6	CD611240	CD611240 56015963H
c 42	85	32.7	545	6	CD611241	CD611241 56015963J
43	82	31.5	922	8	CV811526	CV811526 AGENCOURT
44	77	29.6	560	3	BP341700	BP341700 BP341700
45	77	29.6	566	3	BP377279	BP377279 BP377279

ALIGNMENTS

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DEFINITION  602696515F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4828610 5',
            mRNA sequence.
ACCESSION   BG718473
VERSION     BG718473.1  GI:13997660
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 818)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
            cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
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                     primary library enriched for full-length clones and
                     constructed using the Cap-trapper method (Carninci, in
                     preparation). Library constructed by M. Brownstein
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OM nucleic - nucleic search, using sw model

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

Run on: April 8, 2006, 13:46:44 ; Search time 127.95 Seconds
(without alignments)
3612.096 Million cell updates/sec

Title: US-10-500-173-2
Perfect score: 260
Sequence: 1 gaaacaatgacacaatcagc........gccagagcccaccggccagc 260

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	78	30.0	1501	3	US-09-949-016-3885	Sequence 3885, Ap
4	78	30.0	1504	3	US-09-949-016-185	Sequence 185, Appl
c 5	36.8	14.2	8106	3	US-10-029-517-19	Sequence 19, Appli
6	36	13.8	120	3	US-09-313-294A-4341	Sequence 4341, Ap
7	34.6	13.3	601	3	US-09-949-016-169734	Sequence 169734,
8	34.6	13.3	3510	9	US-09-265-585C-95	Sequence 95, Appl
9	34.6	13.3	5962	9	5386025-5	Patent No. 5386025
c 10	34.6	13.3	5975	2	US-08-404-354B-1	Sequence 1, Appli
c 11	34.6	13.3	5975	2	US-08-314-083B-1	Sequence 1, Appli
c 12	34.6	13.3	5975	2	US-08-435-675B-1	Sequence 1, Appli
c 13	34.6	13.3	5975	3	US-08-336-257A-3	Sequence 3, Appli
c 14	34.6	13.3	5975	3	US-08-884-599-1	Sequence 1, Appli
c 15	34.4	13.2	23187	3	US-09-499-522-1	Sequence 1, Appli
16	33.4	12.8	601	3	US-09-949-016-169736	Sequence 169736,
c 17	33.4	12.8	2400	3	US-08-930-001-1	Sequence 1, Appli
18	33.4	12.8	2400	3	US-09-091-885-1	Sequence 1, Appli
c 19	33.4	12.8	18079	3	US-09-949-016-13344	Sequence 13344, A
c 20	33.4	12.8	99748	3	US-09-949-016-11990	Sequence 11990, A
c 21	33.4	12.8	99749	3	US-09-949-016-16518	Sequence 16518, A
22	33	12.7	342	3	US-09-893-737-93	Sequence 93, Appl
c 23	33	12.7	601	3	US-09-949-016-55187	Sequence 55187, A
c 24	33	12.7	601	3	US-09-949-016-55188	Sequence 55188, A
c 25	33	12.7	601	3	US-09-949-016-169735	Sequence 169735,
c 26	33	12.7	675	3	US-09-252-991A-5532	Sequence 5532, Ap
27	33	12.7	1485	3	US-09-252-991A-5638	Sequence 5638, Ap
28	33	12.7	3321	3	US-09-252-991A-5668	Sequence 5668, Ap
c 29	32.6	12.5	690	3	US-09-252-991A-5557	Sequence 5557, Ap
30	32.4	12.5	4403765	3	US-09-103-840A-2	Sequence 2, Appli
31	32.4	12.5	4411529	3	US-09-103-840A-1	Sequence 1, Appli
c 32	32.2	12.4	7218	2	US-08-232-463-14	Sequence 14, Appl
c 33	32	12.3	10465	3	US-09-949-016-13136	Sequence 13136, A
34	31.8	12.2	601	3	US-09-949-016-40415	Sequence 40415, A
35	31.8	12.2	601	3	US-09-949-016-91943	Sequence 91943, A
36	31.8	12.2	601	3	US-09-949-016-194884	Sequence 194884,
37	31.8	12.2	601	3	US-09-949-002-3572	Sequence 3572, Ap
38	31.8	12.2	601	3	US-09-949-002-6250	Sequence 6250, Ap
39	31.8	12.2	601	3	US-09-949-002-10314	Sequence 10314, A
40	31.8	12.2	1510	2	US-08-300-903A-12	Sequence 12, Appl
41	31.8	12.2	1510	3	US-08-988-197-12	Sequence 12, Appl
42	31.8	12.2	1510	3	US-10-385-072-12	Sequence 12, Appl
43	31.8	12.2	14395	3	US-09-949-016-12247	Sequence 12247, A
44	31.8	12.2	14395	3	US-09-949-016-16357	Sequence 16357, A
c 45	31.8	12.2	14688	3	US-09-949-016-12220	Sequence 12220, A

ALIGNMENTS

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US-09-949-016-11927

; Sequence 11927, Application US/0994016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11927
; LENGTH: 15585
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(15585)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-11927

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

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Perfect score: 260
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Scoring table: IDENTITY_NUC
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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2	260	100.0	260	8	US-10-500-173-2	Sequence 2, Appli
3	260	100.0	333	8	US-10-477-797-3	Sequence 3, Appli
4	260	100.0	333	8	US-10-500-173-3	Sequence 3, Appli
5	143	55.0	1580	6	US-10-062-674-1778	Sequence 1778, Ap
6	135	51.9	1586	5	US-10-084-817-233	Sequence 233, App
7	92	35.4	1517	3	US-09-969-708-354	Sequence 354, App
8	92	35.4	1517	7	US-09-873-367C-655	Sequence 655, App
9	92	35.4	1517	7	US-10-243-425-1209	Sequence 1209, Ap
10	92	35.4	1517	9	US-10-843-641A-655	Sequence 655, App
11	92	35.4	1517	9	US-10-843-641A-7825	Sequence 7825, Ap
12	92	35.4	1517	9	US-10-756-149-3969	Sequence 3969, Ap
13	78	30.0	1504	5	US-10-205-823-69	Sequence 69, Appl
14	78	30.0	1504	8	US-10-788-792-36	Sequence 36, Appl
15	78	30.0	1504	8	US-10-473-974-194	Sequence 194, App
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17	76.2	29.3	156	8	US-10-357-930-35569	Sequence 35569, A
18	76.2	29.3	711	8	US-10-357-930-14461	Sequence 14461, A
c 19	42.8	16.5	455	5	US-10-027-632-270660	Sequence 270660,
c 20	42.8	16.5	455	6	US-10-027-632-270660	Sequence 270660,
c 21	41.6	16.0	455	5	US-10-027-632-270661	Sequence 270661,
c 22	41.6	16.0	455	6	US-10-027-632-270661	Sequence 270661,
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c 24	41	15.8	41	8	US-10-500-173-1	Sequence 1, Appl1
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26	39.4	15.3	425	8	US-09-918-995-17846	Sequence 17846, A
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c 29	37.6	14.5	142299	3	US-10-724-806-14	Sequence 14, Appl
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31	37.4	14.4	3195	6	US-10-285-976-54	Sequence 54, Appl
32	37.4	14.4	3195	6	US-10-295-027-1127	Sequence 1127, Ap
33	37.4	14.4	3195	8	US-10-783-528-48	Sequence 48, Appl
34	37.4	14.4	3195	9	US-10-882-566A-8	Sequence 8, Appl1
c 35	37.4	14.4	3195	10	US-11-051-454-143	Sequence 143, App
c 36	37.4	14.4	3205	8	US-10-723-860-7397	Sequence 7397, Ap
37	37.4	14.4	3206	7	US-10-112-944-6	Sequence 6, Appli
38	37.2	14.3	3740	7	US-10-043-160-4	Sequence 4, Appli
39	37.2	14.3	696	7	US-10-260-238-1452	Sequence 1452, Ap
c 40	36.8	14.2	451	3	US-09-895-828-28	Sequence 28, Appl
c 41	36.8	14.2	451	5	US-10-114-666-28	Sequence 28, Appl
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43	36.8	14.2	8181	8	US-10-447-839A-18	Sequence 18, Appl
c 44	36.8	14.2	8181	8	US-10-778-859-18	Sequence 18, Appl
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; Sequence 2, Application US/10477797
; Publication No. US2004019730BA1
; GENERAL INFORMATION:
; APPLICANT: JAPAN SCIENCE AND TECHNOLOGY CORPORATION
; TITLE OF INVENTION: Replication Vector Showing Cell-Specific Expression
; FILE REFERENCE: K01002PCT
; CURRENT APPLICATION NUMBER: US/10/477,797
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: JP P2001-143999
; PRIOR FILING DATE: 2001-05-14
; NUMBER OF SEQ ID NOS: 16
; SEQ ID NO 2
; LENGTH: 260
; TYPE: DNA
; ORGANISM: Homo sapiens
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Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2

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          Copyright  GenCore version 5.1.7
          Copyright (c) 1993 - 2006 Biocceleration Ltd.

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Pred. No. is the number of results predicted by chance to have a
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SUMMARIES

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6	c	34.8	13.4	13299	14	US-11-124-367A-5011	Sequence 5011, Ap
7	c	34.4	13.2	23187	11	US-11-236-198-1	Sequence 1, Appli
8	c	33.6	12.9	2213	9	US-10-330-773-94	Sequence 94, Appl
9	c	33.6	12.9	26563	9	US-10-330-773-93	Sequence 93, Appl
10	c	33.4	12.8	153376	14	US-11-121-086-5	Sequence 5, Appli
11	c	33.4	12.8	172543	14	US-11-121-086-6	Sequence 6, Appli
12		33.2	12.8	398	11	US-11-116-881A-1686	Sequence 1686, Ap
13		33.2	12.8	22855	14	US-11-124-368A-2908	Sequence 2908, Ap
14	c	33	12.7	1521	14	US-11-136-527-1998	Sequence 1998, Ap
15	c	33	12.7	3752	8	US-10-750-185-28772	Sequence 28772, A
16	c	33	12.7	3752	8	US-10-750-623-28772	Sequence 28772, A
17	c	32.8	12.6	614	6	US-09-925-065A-780929	Sequence 780929,
18	c	32.8	12.6	978	10	US-10-301-480-548844	Sequence 548844,

19	c	32.8	12.6	978	10	US-10-301-480-1162253	Sequence 1162253,
20		32.6	12.5	1380	11	US-11-096-568A-21494	Sequence 21494, A
21	c	32.4	12.5	2514	14	US-11-052-554A-543	Sequence 543, App
22		32.4	12.5	3071	14	US-11-136-527-2592	Sequence 2592, Ap
23		32.4	12.4	98345	14	US-11-112-908-36	Sequence 36, Appl
24		32.2	12.4	670	6	US-09-925-065A-696624	Sequence 696624,
25	c	32.2	12.4	1180	8	US-10-750-185-30591	Sequence 30591, A
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28		32	12.3	656	14	US-11-136-527-1651	Sequence 1651, Ap
29	c	32	12.2	656	14	US-11-136-527-5747	Sequence 5747, Ap
30	c	31.6	12.2	598	8	US-10-750-185-4680	Sequence 4680, Ap
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33		31.6	12.1	191684	14	US-11-121-086-2	Sequence 2, Appli
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36		31.4	11.9	2039	10	US-10-301-480-803085	Sequence 803085,
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ALIGNMENTS

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; Publication No. US20050287544A1
; GENERAL INFORMATION:
; APPLICANT: BERTUCCI, Francois
; APPLICANT: HOULGATTE, Remi
; APPLICANT: BIRNBAUM, Daniel
; TITLE OF INVENTION: GENE EXPRESSION PROFILING OF COLON CANCER WITH DNA ARRAYS
; FILE REFERENCE: 1423-R-03
; CURRENT APPLICATION NUMBER: US/11/000,688
; CURRENT FILING DATE: 2004-12-01
; PRIOR APPLICATION NUMBER: US 60/525,987
; PRIOR FILING DATE: 2003-12-01
; NUMBER OF SEQ ID NOS: 1596
; SOFTWARE: PatentIn version 3.2
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US-11-000-688-1504

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Qy   217 AGCGTCAGTGCCGCCACTGCCCCCCGCCAGAGCCCACCGGCCAGC 260
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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| 4 | 323 | 97.0 | 1221 | 8 | D85611 | D85611 Human smoot |
| c 5 | 308 | 92.5 | 314 | 8 | HS12H4R | Z54537 H.sapiens C |
| c 6 | 261.6 | 78.6 | 224294 | 14 | AC151861 | AC151861 Colobus g |
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| 9 | 259.6 | 78.0 | 178488 | 14 | AC151856 | AC151856 Papio ham |
| 10 | 251.2 | 75.4 | 186803 | 14 | AC151868 | AC151868 Callithri |
| 11 | 248 | 74.5 | 181714 | 14 | AC151893 | AC151893 Aotus nan |
| c 12 | 246.4 | 74.0 | 163264 | 14 | AC151891 | AC151891 Callicebu |
| 13 | 246.4 | 74.0 | 250810 | 14 | AC151886 | AC151886 Saimiri b |
| 14 | 233.4 | 70.1 | 236017 | 14 | AC150437 | AC150437 Lemur cat |
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| c 19 | 195.6 | 58.7 | 207823 | 14 | AC145542 | AC145542 Oryctolag |
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| c 28 | 145.8 | 43.8 | 195294 | 14 | AC051623 | AC051623 Mus muscu |
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| 33 | 141.8 | 42.6 | 1504 | 6 | AX578072 | AX578072 Sequence |
| 34 | 140.8 | 42.6 | 1504 | 8 | U37019 | U37019 Homo sapien |
| 35 | 140.8 | 42.3 | 1521 | 8 | AK223234 | AK223234 Homo sapi |
| 36 | 136.2 | 40.9 | 1496 | 8 | S80560 | S80560 basic calpo |
| 37 | 94.8 | 28.5 | 1123 | 4 | AF323674 | AF323674 Mustela p |
| 38 | 89.4 | 26.8 | 711 | 6 | CQ482594 | CQ482594 Sequence |
| 39 | 87.4 | 26.2 | 485 | 9 | AF123268 | AF123268 Rattus no |
| 40 | 86.6 | 26.0 | 156 | 6 | CQ503702 | CQ503702 Sequence |
| 41 | 84.2 | 25.3 | 3001 | 9 | MMU37071 | U37071 Mus musculu |
| 42 | 82.4 | 24.7 | 164 | 9 | MMCALP02 | U38930 Mus musculu |
| 43 | 76.8 | 23.1 | 1499 | 4 | AY327118 | AY327118 Ovis arie |
| 44 | 75 | 22.5 | 1470 | 9 | SSH1CALA | Z19538 S.scrofa h1 |
| 45 | 72.2 | 21.7 | 1524 | 9 | MMH1CALA | Z19542 M.musculus |

## ALIGNMENTS

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RESULT 1
BD181248

LOCUS       BD181248                 333 bp    DNA     linear   PAT 15-MAY-2003
DEFINITION  Cell specific express replication vector.
ACCESSION   BD181248
VERSION     BD181248.1  GI:30792166
KEYWORDS    JP 2002335965-A/3.
SOURCE      synthetic construct
ORGANISM    synthetic construct
            other sequences; artificial sequences.
REFERENCE   1 (bases 1 to 333)
AUTHORS     Takahashi,K., Yamamura,H. and Miyatake,S.
TITLE       Cell specific express replication vector
JOURNAL     Patent: JP 2002335965-A 3 26-NOV-2002;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT     OS   Artificial Sequence
            PN   JP 2002335965-A/3
            PD   26-NOV-2002
            PF   14-MAY-2001 JP 2001143999
            PI   KATSUHITO TAKAHASHI,HISAKO YAMAMURA,SHINICHI MIYATAKE PC
            C12N15/09,A61K35/76,A61K48/00,A61P35/00,C12N5/10,C12N15/00, PC
            C12N5/00
            CC   Description of Artificial Sequence: Region consist of human
            CC   calponin gene
            CC   promoter and its structural gene fragment
FH   Key             Location/Qualifiers
FT   source          1..333
FEATURES             Location/Qualifiers
     source          1..333
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                     /organism="synthetic construct"
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ORIGIN

Query Match             100.0%;  Score 333;  DB 6;  Length 333;
Best Local Similarity   100.0%;  Pred. No. 7e-72;
Matches  333;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAAACAATGACACAATCAGCTCCCAATACCAAGGGCCTGACATCACAAGGGGAGGGGGAAG 60
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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 9, 2006, 02:04:37 ; Search time 482.692 Seconds
(without alignments)
4597.840 Million cell updates/sec

Title: US-10-500-173-3
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Scoring table: IDENTITY.NUC
Gapop 10.0 , Gapext 1.0

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	333	100.0	333	10	ADC21272	Adc21272 Human cal
2	333	100.0	333	10	ADD68311	Add68311 DNA compr
3	333	100.0	333	10	ADD29395	Add29395 Human cal
4	333	100.0	333	10	AB270046	Abz70046 Human cal
5	276.8	83.1	1206	13	ACN41242	Acn41242 Human dia
6	276.8	83.1	1257	13	ACN41241	Acn41241 Human dia
7	276.8	83.1	1395	13	ACN41239	Acn41239 Human dia
8	276.8	83.1	1395	13	ACN41240	Acn41240 Human dia
9	260	78.1	260	10	ADC21271	Adc21271 Human cel
10	260	78.1	260	10	ADD68310	Add68310 Human ang
11	260	78.1	260	10	ADD29394	Add29394 Antiarter
12	260	78.1	260	10	AB270045	Abz70045 Oligonucl
13	227.8	68.4	1605	12	ADN04009	Adn04009 Antipsori
14	198.8	59.7	1586	2	ADJ56427	Adj56427 Human cDN
15	163.8	49.2	1522	2	AAQ86719	Aaq86719 Carponin
16	163.8	49.2	1522	2	AAT18663	Aat18663 Carponin
17	155.8	46.8	1517	6	ABL62318	Abl62318 Colon ade
18	155.8	46.8	1517	6	ABL69488	Abl69488 Prostate
19	155.8	46.8	1517	6	ABT10830	Abt10830 Human bre
20	141.8	42.6	1499	12	ADQ83552	Adq83552 Human tum
21	141.8	42.6	1504	4	AAD07354	Aad07354 Human DNA
22	141.8	42.6	1504	8	ABZ34836	Abz34836 Coding se
23	141.8	42.6	1504	10	ADR75245	Adr75245 Prostate
24	141.8	42.6	1504	13	ADR99030	Adr99030 Calponin
25	103.6	31.1	425	13	ACH30634	Ach30634 Human tes
26	89.4	26.8	711	5	ABV14470	Abv14470 Human pro
27	86.6	26.0	156	5	ABV35551	Abv35551 Human pro
28	62.4	18.7	538	6	ABN73703	Abn73703 Bovine em
29	57.8	17.4	648	5	ABV05301	Abv05301 Human pro
30	43.6	13.1	120	6	ABX85881	Abx85881 Corn ear-
31	43.4	13.0	1932	6	ABK63774	Abk63774 Rat seque
32	43.4	13.0	1932	10	ADB58375	Adb58375 Toxicity-
33	43.4	13.0	1932	10	ADB52947	Adb52947 Primary r
34	43.2	13.0	1932	13	ADV41198	Adv41198 Rat cardi
35	43.2	13.0	696	12	ADJ40452	Adj40452 Plant cDN
36	41.6	12.5	120	6	ABL71519	Abl71519 Corn tass
37	41.6	12.5	1499	6	ADM86965	Adm86965 Human pro
38	41.2	12.4	283	3	AAC09556	Aac09556 Human sec
39	41.2	12.4	840	14	AEA19761	Aea19761 Novel hum
40	41.2	12.4	1866	12	ADQ64918	Adq64918 Novel hum
41	41.2	12.4	2122	6	ABN95249	Abn95249 Gene #174
42	41.2	12.4	2122	13	ADP54264	Adp54264 Human PRO
43	41.2	12.4	2122	6	ADY14592	Ady14592 DNA encod
44	41.2	12.4	2161	8	ACC46585	Acc46585 Human dit
45	41	12.3	41	10	ADC21270	Adc21270 Human cel

ALIGNMENTS

RESULT 1
ADC21272
ID   ADC21272 standard; DNA; 333 BP.
XX
AC   ADC21272;
XX
DT   18-DEC-2003 (first entry)
XX
DE   Human calponin gene promoter with its structural gene fragment.
XX
KW   human; cell-specific expression vector; cell-specific replication vector;
KW   gene therapy; malignant tumour; liver fibrosis; postoperative stenosis;
KW   organ transplantation; arteriosclerosis; diabetic omentopathy; ds;
KW   calponin; promoter; structural gene fragment.
XX
OS   Homo sapiens.
XX
PN   WO2003057888-A1.
XX
PD   17-JUL-2003.
XX
PF   26-DEC-2002; 2002WO-JP013683.
XX
PR   28-DEC-2001; 2001JP-00402102.
PR   30-AUG-2002; 2002JP-00255395.
XX
PA   (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
PI   Takahashi K, Yamamura H;
XX
DR   WPI; 2003-577527/54.
XX
PT   Cell-specific expression/replication vector containing transcription
PT   initiation regulating domain of human calponin gene, applicable in gene
PT   therapy of malignant tumor lung and liver fibrosis or diabetic
PT   omentopathy.
XX
PS   Claim 4; SEQ ID NO 3; 66pp; Japanese.
XX
CC   The invention comprises a cell-specific expression/replication vector
CC   which does not act on normal cells. The vector of the invention is useful
CC   in gene therapy for the treatment of: malignant tumour, liver fibrosis,

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                    GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on:    April 9, 2006, 02:12:09 ; Search time 3422.44 Seconds
                                      (without alignments)
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters:    82156650

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	227.8	68.4	596	2	BG720683	BG720683 602692572
3	216	64.9	789	3	BI831662	BI831662 603078806
4	176.2	52.9	577	2	BI831410	BI831410 603074509
5	166.8	50.1	300	1	AU099476	AU099476 AU099476
6	166.8	50.1	580	3	BP257909	BP257909 BP257909
7	166.8	50.1	580	3	BP343021	BP343021 BP343021
8	166.8	50.1	581	3	BP216801	BP216801 BP216801
9	166.8	50.1	581	3	BP375335	BP375335 BP375335
10	166.8	50.1	582	3	BP262111	BP262111 BP262111
11	166.8	50.1	582	3	BP311382	BP311382 BP311382
12	166.8	50.1	582	3	BP329165	BP329165 BP329165
13	166.8	50.1	582	3	BP330989	BP330989 BP330989
14	166.8	50.1	582	3	BP331068	BP331068 BP331068
15	166.8	50.1	583	3	BP329772	BP329772 BP329772
16	166.8	50.1	588	3	BP329527	BP329527 BP329527
17	166.8	50.1	791	1	AU136287	AU136287 AU136287
18	166.8	50.1	874	1	AU122686	AU122686 AU122686
19	165.8	49.8	566	3	BP261780	BP261780 BP261780
20	165.8	49.8	778	8	CX756920	CX756920 AGENCOURT
21	165.2	49.8	930	5	BU526756	BU526756 AGENCOURT
22	165.2	49.6	580	3	BP372922	BP372922 BP372922
23	165.2	49.6	583	3	BP330966	BP330966
24	163.6	49.1	582	3	BP206459	BP206459
25	160.8	48.3	581	3	BP328199	BP328199
26	158	47.4	471	7	CN366947	170004241
27	155.8	46.8	582	3	BP377953	BP377953
28	154.8	46.5	646	7	CN366953	170005999
29	154.8	46.5	1444	4	CR620483	full-leng
30	153.8	46.2	742	8	CX752039	AGENCOURT
31	152	45.6	762	8	CX753789	AGENCOURT
32	152	45.6	1086	3	BM553077	AGENCOURT
33	151.8	45.6	660	1	AL046845	DKFZp586B
34	151.8	45.6	706	1	AL046846	DKFZp586B
35	151.2	45.4	714	1	AL046924	DKFZp586H
36	150.8	45.3	996	1	BI771104	603059679
37	149.8	45.0	700	1	AL533558	AL533558
38	149.8	45.0	942	5	BU838479	AGENCOURT
39	148.8	44.7	545	6	CD611240	56015963H
c 40	148.8	44.7	545	6	CD611241	56015963J
41	143.6	43.1	922	8	CV811526	AGENCOURT
42	141.2	42.4	832	5	BX374338	BX374338
43	140.8	42.3	560	3	BP341700	BP341700
44	140.8	42.3	566	3	BP377279	BP377279
45	140.8	42.3	580	3	BP372484	BP372484

ALIGNMENTS

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DEFINITION  602696515F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4828610 5',
            mRNA sequence.
ACCESSION   BG718473
VERSION     BG718473.1    GI:13397660
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 818)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
            cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
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                     preparation). Library constructed by M. Brownstein
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                GenCore version 5.1.7
        Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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5	45	13.5	33753	3	US-09-949-016-15741	Sequence 15741, A
6	45	13.5	33756	3	US-09-949-016-12006	Sequence 12006, A
7	44.4	13.3	15273	3	US-09-949-016-12356	Sequence 12356, A
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9	43.6	13.1	120	3	US-09-313-294A-4341	Sequence 4341, Ap
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12	41.2	12.4	2122	3	US-09-949-016-1599	Sequence 1599, Ap
13	40.6	12.2	1589	3	US-09-949-016-3999	Sequence 3999, Ap
14	40.6	12.2	1607	3	US-09-949-016-264	Sequence 264, App
15	36.8	11.1	8186	3	US-10-029-517-19	Sequence 19, Appl
16	36.2	10.9	23187	3	US-09-499-522-1	Sequence 1, Appli
17	34.6	10.4	601	3	US-09-949-016-169734	Sequence 169734,
18	34.6	10.4	3510	3	US-09-265-585C-95	Sequence 95, Appl
19	34.6	10.4	5962	9	5386025-5	Patent No. 5386025
c 20	34.6	10.4	5975	2	US-08-404-354B-1	Sequence 1, Appli
c 21	34.6	10.4	5975	2	US-08-314-083B-1	Sequence 1, Appli
c 22	34.6	10.4	5975	2	US-08-435-675B-1	Sequence 1, Appli
c 23	34.6	10.4	5975	3	US-08-336-257A-3	Sequence 3, Appli
c 24	34.6	10.4	5975	3	US-08-884-599-1	Sequence 1, Appli
c 25	34.4	10.3	598	3	US-09-669-751-32	Sequence 32, Appl
26	34.4	10.3	2065	3	US-09-902-540-7188	Sequence 7188, Ap
27	34.4	10.3	5051	3	US-09-902-540-667	Sequence 667, App
28	34.2	10.3	114426	3	US-09-949-016-15078	Sequence 15078, A
29	33.8	10.2	15756	3	US-09-949-016-13607	Sequence 13607, A
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c 31	33.6	10.1	14688	3	US-09-949-016-12220	Sequence 12220, A
c 32	33.6	10.1	14797	3	US-09-949-016-13719	Sequence 13719, A
33	33.6	10.1	15778	3	US-09-949-016-13538	Sequence 13538, A
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c 41	33.4	10.0	99748	3	US-09-949-016-11990	Sequence 11990, A
c 42	33.4	10.0	99749	3	US-09-949-016-16518	Sequence 16518, A
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c 45	33	9.9	601	3	US-09-949-016-55187	Sequence 55187, A

ALIGNMENTS

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; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER:
;  CURRENT FILING DATE:
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
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;  ORGANISM: Human
;  FEATURE:
;  NAME/KEY: misc_feature
;  LOCATION: (1)...(15585)
;  OTHER INFORMATION: n = A,T,C or G
US-09-949-016-11927

Query Match             99.5%;  Score 331.4;  DB 3;  Length 15585;
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Qy         61 GCAGCTGAGGTTGTGGGGGAGGTGCCCGCCCTTGGCAGGCCCCTACAGCCAATGGAA 120
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Qy        121 CGGGCCCTGGAAGAGACCCGGGTCGCCTCCGGAGCTTCAAAAACATGTGAGGAGGGAGAG 180
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Qy        181 TGTGCAGACGGAACTTCAGCCAGTGTTCTCAGCGTCAGTGCCGCCACTGCCCCC 240
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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 9, 2006, 02:22:52 ; Search time 782.077 seconds
                                          (without alignments)
                                          3521.011 Million cell updates/sec

Title: US-10-500-173-3
Perfect score: 333
Sequence: 1 gaaacaatgacacaatcagc..........taagaacaaggtaggggtgg 333

Scoring table: IDENTITY_NUC
                  Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 413468905 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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1	333	100.0	333	8	US-10-477-797-3	Sequence 3, Appli
2	333	100.0	333	8	US-10-500-173-3	Sequence 3, Appli
3	260	78.1	260	8	US-10-477-797-2	Sequence 2, Appli
4	260	78.1	260	8	US-10-500-173-2	Sequence 2, Appli
5	206.8	62.1	1580	6	US-10-062-674-1778	Sequence 1778, Ap
6	198.8	59.7	1586	5	US-10-084-817-233	Sequence 233, App
7	155.8	46.8	1517	3	US-09-969-708-354	Sequence 354, App
8	155.8	46.8	1517	3	US-09-873-367C-655	Sequence 655, App
9	155.8	46.8	1517	7	US-10-240-425-1209	Sequence 1209, Ap
10	155.8	46.8	1517	9	US-10-843-641A-655	Sequence 655, App
11	155.8	46.8	1517	9	US-10-843-641A-7825	Sequence 7825, Ap
12	155.8	46.8	1517	9	US-10-756-149-3969	Sequence 3969, Ap
13	141.8	42.6	1504	5	US-10-205-823-69	Sequence 69, Appl
14	141.8	42.6	1504	8	US-10-788-792-36	Sequence 36, Appl
15	141.8	42.6	1504	8	US-10-473-974-194	Sequence 194, App
16	141.8	42.6	1504	10	US-11-051-454-69	Sequence 69, Appl
17	103.6	31.1	425	3	US-09-918-995-17846	Sequence 17846, A
18	89.4	26.8	711	8	US-10-357-930-14461	Sequence 14461, A
19	86.6	26.0	156	8	US-10-357-930-35569	Sequence 35569, A
20	62.4	18.7	538	3	US-09-876-143-638	Sequence 638, App
21	57.8	17.4	648	8	US-10-357-930-5292	Sequence 5292, Ap
22	53	15.9	359	6	US-10-062-674-535	Sequence 535, App
23	43.4	13.0	1932	3	US-09-917-800A-1681	Sequence 1681, Ap
24	43.2	13.0	696	7	US-10-260-238-1452	Sequence 1452, Ap
25	42.8	12.9	455	5	US-10-027-632-270660	Sequence 270660,
26	42.8	12.9	455	5	US-10-027-632-270660	Sequence 270660,
27	41.6	12.5	120	3	US-09-294-093B-893	Sequence 893, App
28	41.6	12.5	455	6	US-10-027-632-270661	Sequence 270661,
29	41.6	12.5	455	6	US-10-027-632-270661	Sequence 270661,
30	41.2	12.4	1499	7	US-10-112-944-58	Sequence 58, Appl
31	41.2	12.4	2122	3	US-09-880-107-1747	Sequence 1747, Ap
32	41	12.3	41	8	US-10-477-797-1	Sequence 1, Appli
33	41	12.3	41	8	US-10-500-173-1	Sequence 1, Appli
34	41	12.3	127	3	US-09-294-093B-5323	Sequence 5323, Ap
35	40.8	12.3	158001	7	US-10-211-179-11	GENERAL INFORMATI
36	40.6	12.2	419	3	US-09-960-352-12371	Sequence 12371, A
37	40.6	12.2	648	3	US-09-969-034-2416	Sequence 2416, Ap
38	40.6	12.2	1607	6	US-09-795-651-94	Sequence 94, Appl
39	40.6	12.2	1607	6	US-10-133-937-43	Sequence 43, Appl
40	40.6	12.2	1607	6	US-10-172-118-679	Sequence 679, App
41	40.6	12.2	1607	6	US-10-159-563-43	Sequence 43, Appl
42	40.6	12.2	1607	7	US-10-342-887-679	Sequence 679, App
43	40.6	12.2	1607	9	US-10-756-149-40	Sequence 40, Appl
44	37.6	11.3	142299	9	US-09-911-077A-14	Sequence 14, Appl
45	37.6	11.3	142299	8	US-10-724-806-14	Sequence 14, Appl

ALIGNMENTS

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; Sequence 3, Application US/10477797
; Publication No. US2004019730A1
; GENERAL INFORMATION:
; APPLICANT: JAPAN SCIENCE AND TECHNOLOGY CORPORATION
; TITLE OF INVENTION: Replication Vector Showing Cell-Specific Expression
; FILE REFERENCE: K01002PCT
; CURRENT APPLICATION NUMBER: US/10/477,797
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: JP P2001-143999
; PRIOR FILING DATE: 2001-05-14
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
; LENGTH: 333
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Region consist
; OTHER INFORMATION: of human calponin gene promoter and its structural
; OTHER INFORMATION: gene fragment
US-10-477-797-3

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              GenCore version 5.1.7
       Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on:   April 9, 2006, 02:36:12 ; Search time 614.527 Seconds
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Title:            US-10-500-173-3
Perfect score:    333
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Scoring table:    IDENTITY_NUC
                  Gapop 10.0 , Gapext 1.0

Searched:         9267905 seqs, 2000278028 residues

Total number of hits satisfying chosen parameters:      18535810

Minimum DB seq length: 0
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Post-processing:  Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	227.8	68.4	1605	14	US-11-000-688-1504	Sequence 1504, Ap
2	141.8	42.6	1504	11	US-11-245-147-194	Sequence 194, App
3	66.2	19.9	1498	14	US-11-136-527-3031	Sequence 3031, Ap
4	44.6	13.4	2271	14	US-11-136-527-2536	Sequence 2536, Ap
5	44.4	13.3	168516	14	US-11-121-086-3	Sequence 3, Appli
c 6	40.6	12.2	736	8	US-10-750-185-61962	Sequence 61962, A
c 7	40.6	12.2	736	8	US-10-750-623-61962	Sequence 61962, A
8	40.2	12.2	1607	14	US-11-000-688-1008	Sequence 1008, Ap
9	40.2	12.1	1400	14	US-11-136-527-7127	Sequence 7127, Ap
c 10	36.8	11.1	1084	9	US-10-517-696-82	Sequence 82, Appl
c 11	36.8	11.1	1582	11	US-11-050-857-464	Sequence 464, Appl
c 12	36.8	11.1	1582	11	US-11-043-806-59	Sequence 59, Appli
c 13	36.2	10.9	23187	11	US-11-236-198-1	Sequence 1, Appli
14	35.8	10.8	627	10	US-10-301-480-239363	Sequence 239363,
c 15	35.8	10.8	627	10	US-10-301-480-852772	Sequence 852772,
16	35.8	10.8	635	6	US-09-925-065A-144853	Sequence 144853,
17	35.8	10.8	780	10	US-10-301-480-542693	Sequence 542693,
18	35.8	10.8	780	10	US-10-301-480-1156102	Sequence 1156102
c 19	34.8	10.5	13299	14	US-11-124-367A-5011	Sequence 5011, Ap
20	33.6	10.1	2213	9	US-10-330-773-94	Sequence 94, Appl
21	33.6	10.1	22855	14	US-11-124-368A-2908	Sequence 2908, Ap
22	33.6	10.1	26563	9	US-10-330-773-93	Sequence 93, Appl
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c 24	33.4	10.0	153376	14	US-11-121-086-5	Sequence 5, Appli
c 25	33.2	10.0	172543	14	US-11-121-086-6	Sequence 6, Appli
26	33.2		398	11	US-11-116-881A-1686	Sequence 1686, Ap
c 27	33	9.9	1521	14	US-11-136-527-1998	Sequence 1998, Ap
28	33	9.9	3752	8	US-10-750-185-28772	Sequence 28772, A
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31	32.8	9.8	656	14	US-11-136-527-1651	Sequence 1651, Ap
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c 37	32.4	9.7	2514	14	US-11-052-554A-543	Sequence 543, App
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c 41	32.2	9.7	1180	8	US-10-750-185-30591	Sequence 30591, A
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ALIGNMENTS

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; Sequence 1504, Application US/11000688
; Publication No. US20050287544A1
; GENERAL INFORMATION:
; APPLICANT: BERTUCCI, Francois
; APPLICANT: HOULGATTE, Remi
; APPLICANT: BIRNBAUM, Daniel
; TITLE OF INVENTION: GENE EXPRESSION PROFILING OF COLON CANCER WITH DNA ARRAYS
; FILE REFERENCE: 1423-R-03
; CURRENT APPLICATION NUMBER: US/11/000,688
; CURRENT FILING DATE: 2004-12-01
; PRIOR APPLICATION NUMBER: US 60/525,987
; PRIOR FILING DATE: 2003-12-01
; NUMBER OF SEQ ID NOS: 1596
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 1504
; LENGTH: 1605
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial sequences:primer
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1605)
; OTHER INFORMATION: calponin 1, basic, smooth muscle(CNN1) gene.
US-11-000-688-1504

Query Match             68.4%;  Score 227.8;  DB 14;  Length 1605;
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Qy   217 AGGTTCAGTGCCGCCACTGCCCCCGCCAGACCCGCAGACCCACCGGCGCATGTCCTCTGTTCTCACT 276
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